Figure S1 - Multidimensional scaling plot with 4 individuals where distance between samples was calculated using the 500 genes with higher dispersion between each sample pair. Distance between samples is the Euclidian distance (average root-mean-square) of the 500 genes' absolute log 2 fold change between samples. Letters identify each individual sample, and colors identify each molting stage.

Figure S2 - Multidimensional scaling plot with 3 individuals where distance between samples was calculated using the 500 genes with higher dispersion between each sample pair. Distance between samples is the Euclidian distance (average root-mean-square) of the 500 genes' absolute log 2 fold change between samples. Letters identify each individual sample, and colors identify each molting stage.
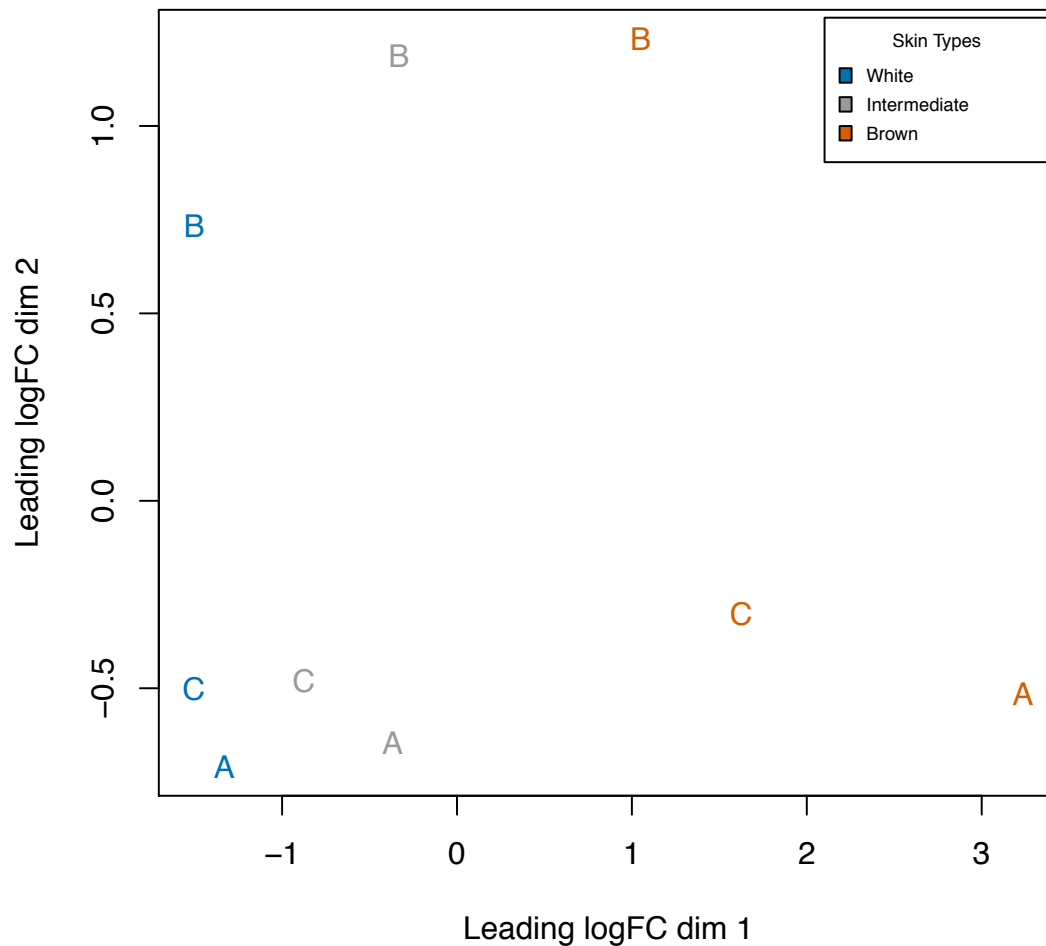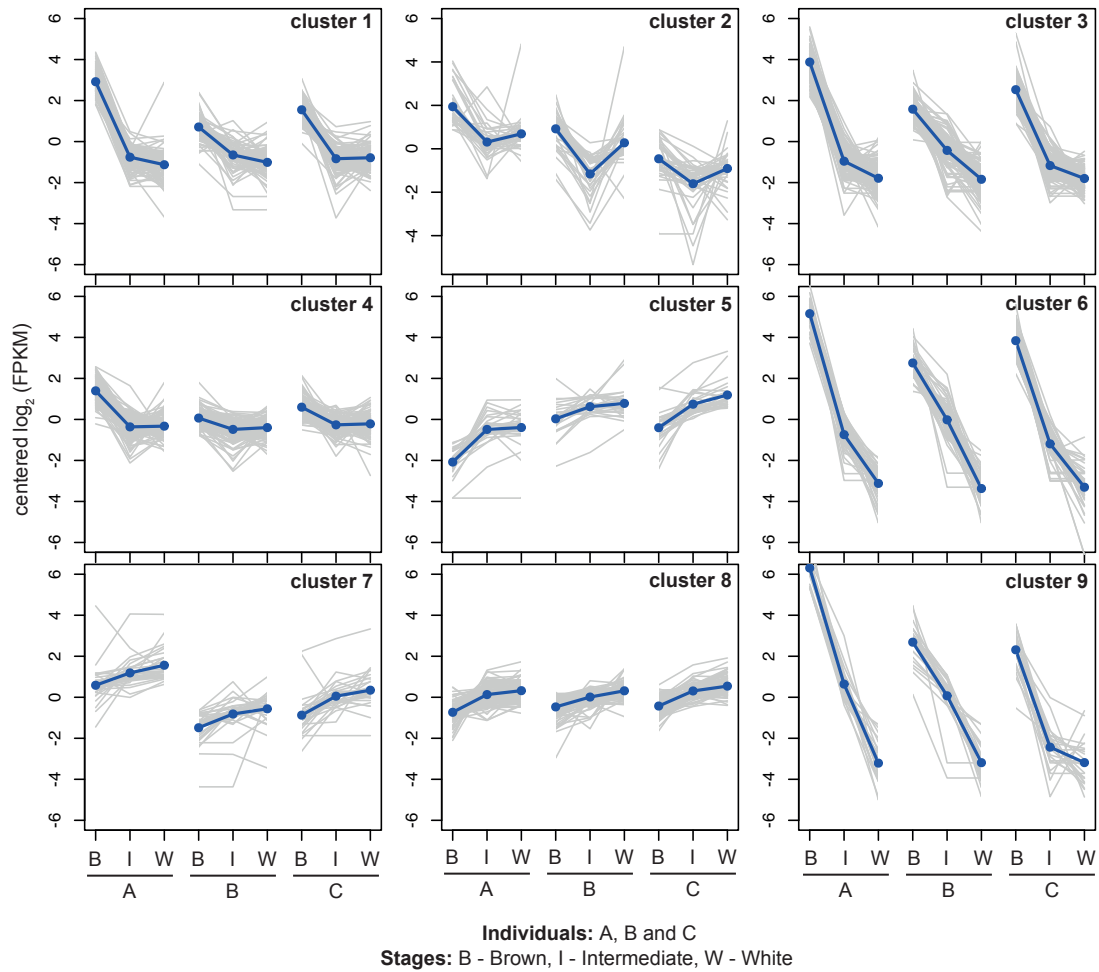
Individuals: A, B and C
Stages: B - Brown, I - Intermediate, W - White

Figure S3 - Clusters are resultant from PAM clustering of individual gene expression levels for k=9. The average expression level for the group of genes in each cluster is displayed in black. Letters A, B and C represent mountain hare individuals and letters B, I and W represent the "brown", "intermediate" and "white" molting stages, respectively.
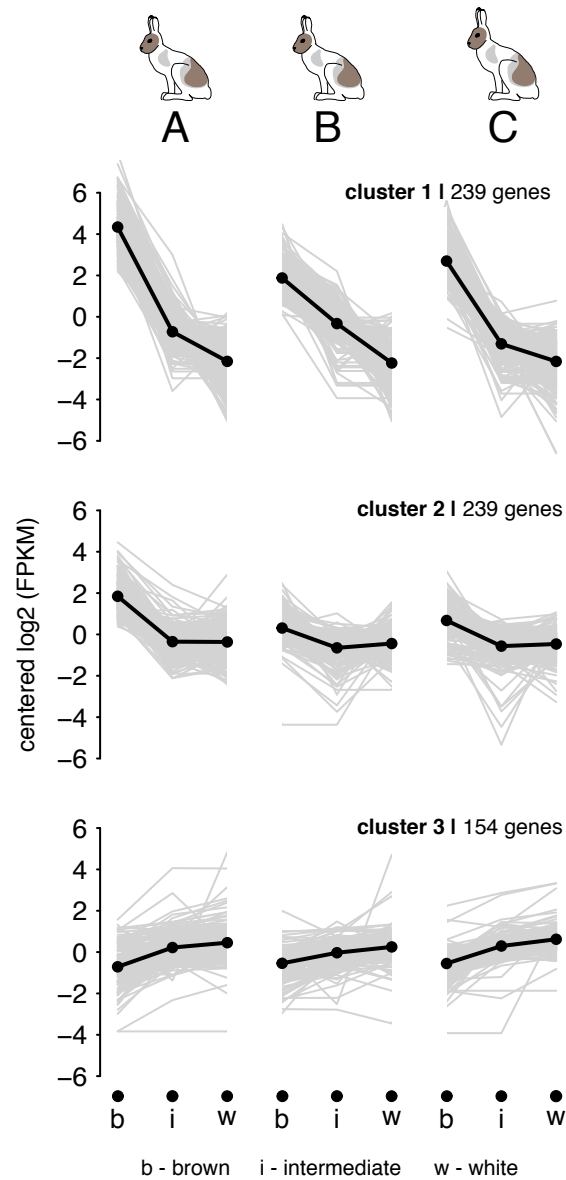
Figure S4 - Clusters are resultant from PAM clustering of individual gene expression levels for k=3. The average expression level for the group of genes in each cluster is displayed in black. Letters A, B and C represent mountain hare individuals and letters B, I and W represent the "brown", "intermediate" and "white" molting stages, respectively.

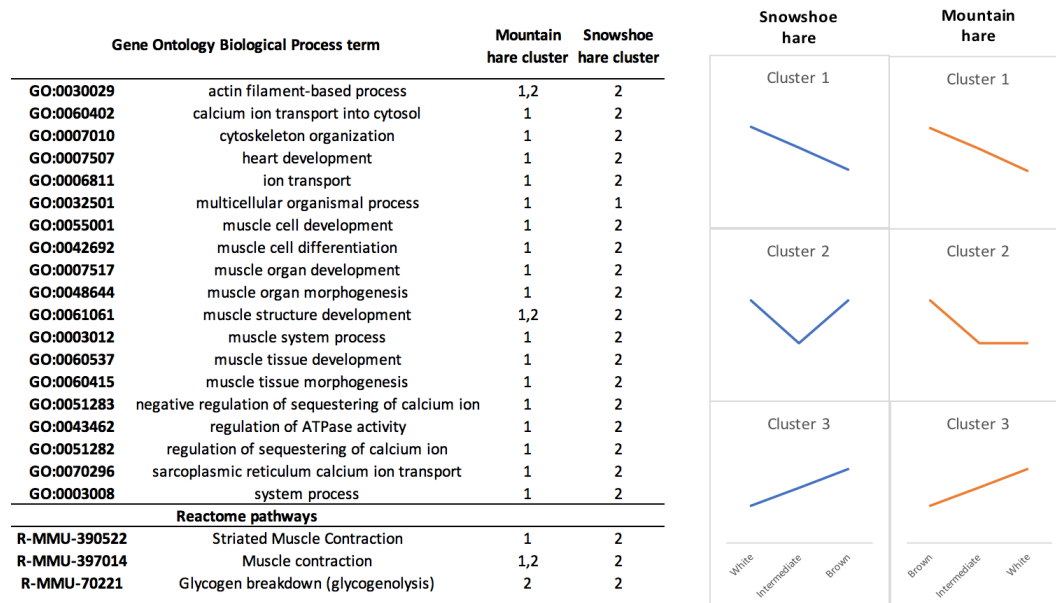| Gene Ontology Biological Process term		Mountain hare cluster	Snowshoe hare cluster
GO:0030029	actin filament-based process	1,2	2
GO:0060402	calcium ion transport into cytosol	1	2
GO:0007010	cytoskeleton organization	1	2
GO:0007507	heart development	1	2
GO:0006811	ion transport	1	2
GO:0032501	multicellular organismal process	1	1
GO:0055001	muscle cell development	1	2
GO:0042692	muscle cell differentiation	1	2
GO:0007517	muscle organ development	1	2
GO:0048644	muscle organ morphogenesis	1	2
GO:0061061	muscle structure development	1,2	2
GO:0003012	muscle system process	1	2
GO:0060537	muscle tissue development	1	2
GO:0060415	muscle tissue morphogenesis	1	2
GO:0051283	negative regulation of sequestering of calcium ion	1	2
GO:0043462	regulation of ATPase activity	1	2
GO:0051282	regulation of sequestering of calcium ion	1	2
GO:0070296	sarcoplasmic reticulum calcium ion transport	1	2
GO:0003008	system process	1	2
Reactome pathways			
R-MMU-390522	Striated Muscle Contraction	1	2
R-MMU-397014	Muscle contraction	1,2	2
R-MMU-70221	Glycogen breakdown (glycogenolysis)	2	2

Figure S5 - Functional overlap between mountain hare Fall molt and snowshoe hare Spring molt dataset. Overlapping Gene Ontology Biological Process term and REACTOME pathway and the clusters where they are enriched in both species datasets.
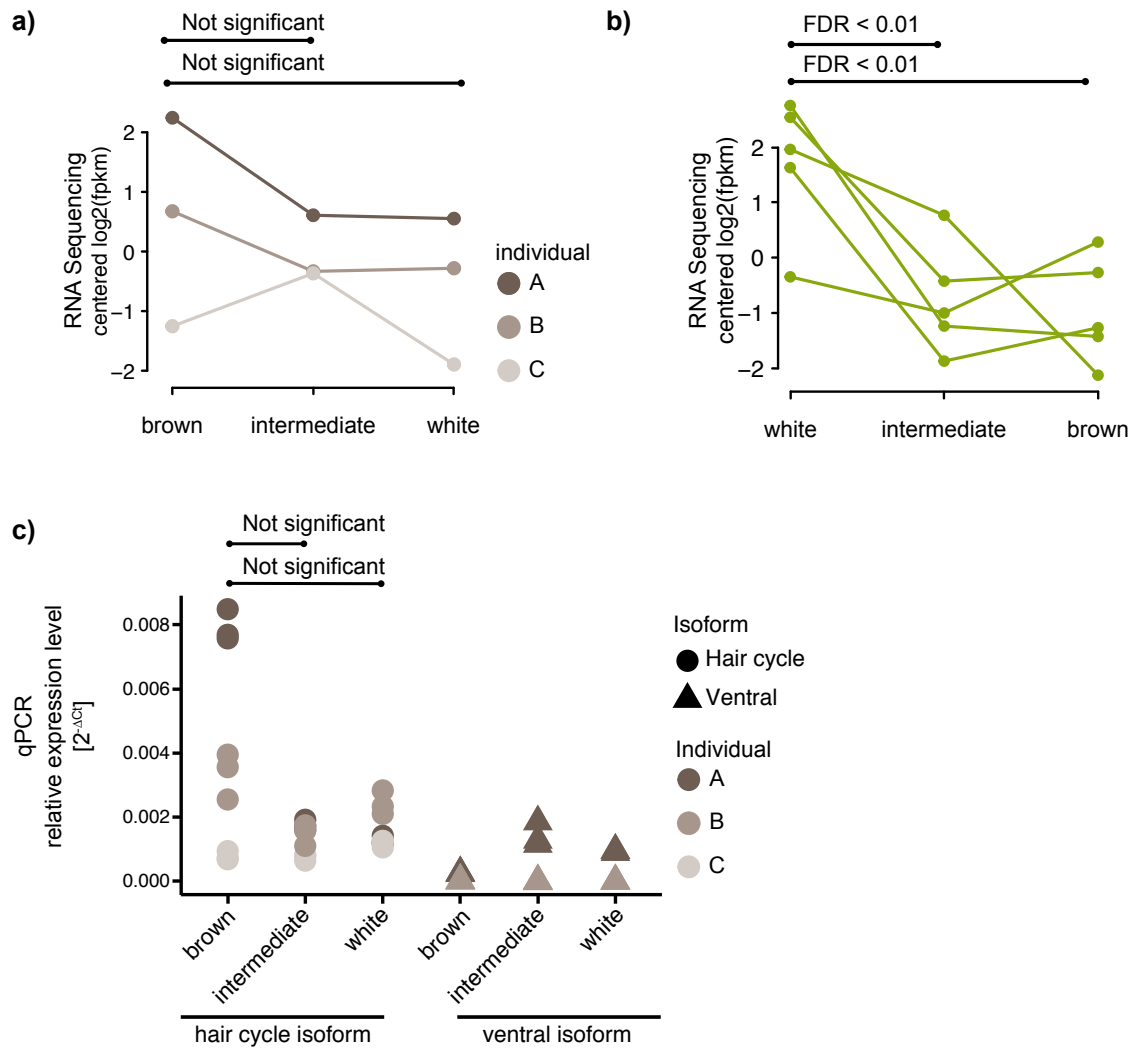
Figure S6 – The expression of candidate agouti signaling peptide (*ASIP*) gene across the autumn molt of (A, C) mountain hares (this work) and (B) spring molt of snowshoe hares (recalculated from Ferreira et al. 2017). For both species (A, B), expression levels are shown in mean centered log2 FPKM for all individuals in each dataset, derived from RNA-sequencing. For mountain hares, (C) relative expression levels estimated from qPCR ($2^{-\Delta Ct}$) for the *ASIP* hair cycle and ventral isoform are shown for individuals and tissue types, using *ACTB* as a reference gene.